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Fig.1

```
GTTTCAGGCA GCGCTGCGTC CTGCTGCGCA CGTGGGAAGC CCTGGCCCCG GCCACCCCCG CGATGCCGCG    70
CGCTCCCCGC TGCCGAGCCG TGCGCTCCCT GCTGCGCAGC CACTACCGCG AGGTGCTGCC GCTGGCCACG   140
TTCGTGCGGC GCCTGGGGCC CCAGGGCTGG CGGCTGGTGC AGCGCGGGGA CCCGGCGGCT TTCCGCGCGC   210
TGGTGGCCCA GTGCCTGGTG TGCGTGCCCT GGGACGCACG GCCGCCCCCC GCCGCCCCCT CCTTCCGCCA   280
GGTGTCCTGC CTGAAGGAGC TGGTGGCCCG AGTGCTGCAG AGGCTGTGCG AGCGCGGCGC GAAGAACGTG   350
CTGGCCTTCG GCTTCGCGCT GCTGGACGGG GCCCGCGGGG GCCCCCCCGA GGCCTTCACC ACCAGCGTGC   420
GCAGCTACCT GCCCAACACG GTGACCGACG CACTGCGGGG GAGCGGGGCG TGGGGGCTGC TGCTGCGCCG   490
CGTGGGCGAC GACGTGCTGG TTCACCTGCT GGCACGCTGC GCGCTCTTTG TGCTGGTGGC TCCCAGCTGC   560
GCCTACCAGG TGTGCGGGCC GCCGCTGTAC CAGCTCGGCG CTGCCACTCA GGCCCGGCCC CCGCCACACG   630
CTAGTGGACC CCGAAGGCGT CTGGGATGCG AACGGGCCTG GAACCATAGC GTCAGGGAGG CCGGGGTCCC   700
CCTGGGCCTG CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC GTTGCCCAAG   770
AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC CCGTTGGGCA GGGGTCCTGG GCCCACCCGG   840
GCAGGACGCG TGGACCGAGT GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC   910
CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG GCCGCCAGCA CCACGCGGGC   980
CCCCCATCCA CATCGCGGCC ACCACGTCCC TGGGACACGC CTTGTCCCCC GGTGTACGCC GAGACCAAGC  1050
ACTTCCTCTA CTCCTCAGGC GACAAGGAGC AGCTGCGGCC CTCCTTCCTA CTCAGCTCTC TGAGGCCCAG  1120
CCTGACTGGC GCTCGGAGGC TCGTGGAGAC CATCTTTCTG GGTTCCAGGC CCTGGATGCC AGGGACTCCC  1190
GTTCATCTCC CTGGGGAAGC ATGCCAAGCT CTCGCTGCAG GAGCTGACGT GGAAGATGAG CGTGCGGGAC  1260
TGCGCTTGGC TGCGCAGGAG CCCAGGGGTT GGCTGTGTTC CGGCCGCAGA GCACCGTCTG CGTGAGGAGA  1330
TCCTGGCCAA GTTCCTGCAC TGGCTGATGA GTGTGTACGT CGTCGAGCTG CTCAGGTCTT TCTTTTATGT  1400
CACGGAGACC ACGTTTCAAA AGAACAGGCT CTTTTTCTAC CGGAAGAGTG TCTGGAGCAA GTTGCAAAGC  1470
ATTGGAATCA GACAGCACTT GAAGAGGGTG CAGCTGCGGG AGCTGTCGGA AGCAGAGGTC AGGCAGCATC  1540
GGGAAGCCAG GCCCGCCCTG CTGACGTCCA GACTCCGCTT CATCCCCAAG CCTGACGGGC TGCGGCCGAT  1610
TGTGAACATG GACTACGTCG TGGGAGCCAG AACGTTCCGC AGAGAAAAGA GGGCCGAGCG TCTCACCTCG  1680
AGGGTGAAGG CACTGTTCAG CGTGCTCAAC TACGAGCGGG CGCGGCGCCC CGGCCTCCTG GGCGCCTCTG  1750
TGCTGGGCCT GGACGATATC CACAGGGCCT GGCGCACCTT CGTGCTGCGT GTGCGGGCCC AGGACCCGCC  1820
GCCTGAGCTG TACTTTGTCA AGGTGGATGT GACGGGCGCG TACGACACCA TCCCCCAGGA CAGGCTCACG  1890
GAGGTCATCG CCAGCATCAT CAAACCCCAG AACACGTACT GCGTGCGTCG GTATGCCGTG GTCCAGAAGG  1960
CCGCCCATGG GCACGTCCGC AAGGCCTTCA AGAGCCACGT CTCTACCTTG ACAGACCTCC AGCCGTACAT  2030
GCGACAGTTC GTGGCTCACC TGCAGGAGAC CAGCCCGCTG AGGGATGCCG TCGTCATCGA GCAGAGCTCC  2100
TCCCTGAATG AGGCCAGCAG TGGCCTCTTC GACGTCTTCC TACGCTTCAT GTGCCACCAC GCCGTGCGCA  2170
TCAGGGGCAA GTCCTACGTC CAGTGCCAGG GGATCCCGCA GGGCTCCATC CTCTCCACGC TGCTCTGCAG  2240
CCTGTGCTAC GGCGACATGG AGAACAAGCT GTTTGCGGGG ATTCGGCGGG ACGGGCTGCT CCTGCGTTTG  2310
GTGGATGATT TCTTGTTGGT GACACCTCAC CTCACCCACG CGAAAACCTT CCTCAGGACC CTGGTCCGAG  2380
GTGTCCCTGA GTATGGCTGC GTGGTGAACT TGCGGAAGAC AGTGGTGAAC TTCCCTGTAG AAGACGAGGC  2450
CCTGGGTGGC ACGGCTTTTG TTCAGATGCC GGCCCACGGC CTATTCCCCT GGTGCGGCCT GCTGCTGGAT  2520
ACCCGGACCC TGGAGGTGCA GAGCGACTAC TCCAGCTATG CCCGGACCTC CATCAGAGCC AGTCTCACCT  2590
TCAACCGCGG CTTCAAGGCT GGGAGGAACA TGCGTCGCAA ACTCTTTGGG GTCTTGCGGC TGAAGTGTCA  2660
CAGCCTGTTT CTGGATTTGC AGGTGAACAG CCTCCAGACG GTGTGCACCA ACATCTACAA GATCCTCCTG  2730
CTGCAGGCGT ACAGGTTTCA CGCATGTGTG CTGCAGCTCC CATTTCATCA GCAAGTTTGG AAGAACCCCA  2800
CATTTTTCCT GCGCGTCATC TCTGACACGG CCTCCCTCTG CTACTCCATC CTGAAAGCCA AGAACGCAGG  2870
GATGTCGCTG GGGGCCAAGG GCGCCGCCGG CCCTCTGCCC TCCGAGGCCG TGCAGTGGCT GTGCCACCAA  2940
GCATTCCTGC TCAAGCTGAC TCGACACCGT GTCACCTACG TGCCACTCCT GGGGTCACTC AGGACAGCCC  3010
AGACGCAGCT GAGTCGGAAG CTCCCGGGGA CGACGCTGAC TGCCCTGGAG GCCGCAGCCA ACCCGGCACT  3080
GCCCTCAGAC TTCAAGACCA TCCTGGACTG ATGGCCACCC GCCCACAGCC AGGCCGAGAG CAGACACCAG  3150
CAGCCCTGTC ACGCCGGGCT CTACGTCCCA GGGAGGGAGG GGCGGCCCAC ACCCAGGCCC GCACCGCTGG  3220
GAGTCTGAGG CCTGAGTGAG TGTTTGGCCG AGGCCTGCAT GTCCGGCTGA AGGCTGAGTG TCCGGCTGAG  3290
GCCTGAGCGA GTGTCCAGCC AAGGGCTGAG TGTCCAGCAC ACCTGCCGTC TTCACTTCCC CACAGGCTGG  3360
CGCTCGGCTC CACCCCAGGG CCAGCTTTTC CTCACCAGGA GCCCGGCTTC CACTCCCCAC ATAGGAATAG  3430
TCCATCCCCA GATTCGCCAT TGTTCACCCC TCGCCCTGCC CTCCTTTGCC TTCCACCCCC ACCATCCAGG  3500
TGGAGACCCT GAGAAGGACC CTGGGAGCTC TGGGAATTTG GAGTGACCAA AGGTGTGCCC TGTACACAGG  3570
CGAGGACCCT GCACCTGGAT GGGGGTCCCT GTGGGTCAAA TTGGGGGGAG GTGCTGTGGG AGTAAAATAC  3640
TGAATATATG AGTTTTTCAG TTTTGAAAAA AAAAAAAAAA AAAAAAAAAA AA                      3690
```

Fig. 2

```
MPRAPRCRAV RSLLRSHYRE VLPLATFVRR LGPQGWRLVQ RGDPAAFRAL    50
VAQCLVCVPW DARPPPAAPS FRQVSCLKEL VARVLQRLCE RGAKNVLAFG   100
FALLDGARGG PPEAFTTSVR SYLPNTVTDA LRGSGAWGLL LRRVGDDVLV   150
HLLARCALFV LVAPSCAYQV CGPPLYQLGA ATQARPPPHA SGPRRRLGCE   200
RAWNHSVREA GVPLGLPAPG ARRRGGSASR SLPLPKRPRR GAAPEPERTP   250
VGQGSWAHPG RTRGPSDRGF CVVSPARPAE EATSLEGALS GTRHSHPSVG   300
RQHHAGPPST SRPPRPWDTP CPPVYAETKH FLYSSGDKEQ LRPSFLLSSL   350
RPSLTGARRL VETIFLGSRP WMPGTPRRLP RLPQRYWQMR PLFLELLGNH   400
AQCPYGVLLK THCPLRAAVT PAAGVCAREK PQGSVAAPEE EDTDPRRLVQ   450
LLRQHSSPWQ VYGFVRACLR RLVPPGLWGS RHNERRFLRN TKKFISLGKH   500
AKLSLQELTW KMSVRDCAWL RRSPGVGCVP AAEHRLREEI LAKFLHWLMS   550
VYVVELLRSF FYVTETTFQK NRLFFYRKSV WSKLQSIGIR QHLKRVQLRE   600
LSEAEVRQHR EARPALLTSR LRFIPKPDGL RPIVNMDYVV GARTFRREKR   650
AERLTSRVKA LFSVLNYERA RRPGLLGASV LGLDDIHRAW RTFVLRVRAQ   700
DPPPELYFVK VDVTGAYDTI PQDRLTEVIA SIIKPQNTYC VRRYAVVQKA   750
AHGHVRKAFK SHVSTLTDLQ PYMRQFVAHL QETSPLRDAV VIEQSSSLNE   800
ASSGLFDVFL RFMCHHAVRI RGKSYVQCQG IPQGSILSTL LCSLCYGDME   850
NKLFAGIRRD GLLLRLVDDF LLVTPHLTHA KTFLRTLVRG VPEYGCVVNL   900
RKTVVNFPVE DEALGGTAFV QMPAHGLFPW CGLLLDTRTL EVQSDYSSYA   950
RTSIRASLTF NRGFKAGRNM RRKLFGVLRL KCHSLFLDLQ VNSLQTVCTN  1000
IYKILLLQAY RFHACVLQLP FHQQVWKNPT FFLRVISDTA SLCYSILKAK  1050
NAGMSLGAKG AAGPLPSEAV QWLCHQAFLL KLTRHRVTYV PLLGSLRTAQ  1100
TQLSRKLPGT TLTALEAAAN PALPSDFKTI LD                     1132
```

Fig. 3

Fig. 4

Lipman-Pearson Protein Alignment
Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>129)	Seq2(1>150)	Similarity	Gap	Gap	Consensus
PHTC.PRO	P123.PRO	Index	Number	Length	Length
(2>124)	(1>117)	31.5	4	6	123

```
                 ↓10        ↓20        ↓30        ↓40        ↓50        ↓60        ↓70        ↓80
PHTC.PRO KFLHWLMSVYYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLR
         K:L:W:..  VV.L:R.FFYVTE     :: ::YRK::W. : .::I .:LK:  L :V E EV :::. . :: .::LR
P123.PRO KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEV-EEWKKSLGFAPGKLR
                  ↑10        ↑20        ↑30        ↑40        ↑50        ↑60        ↑70

                 ↓90        ↓100       ↓110       ↓120
PHTC.PRO FIPKPDGLRPIVNMDYYVGARTFRREKRAERLTSRVKALFSVLNYERA
         :IPK ..:RPI  M.:  . :. ..:::::LT:..K L S L  .
P123.PRO LIPKKTTFRPI--MTF--NKKIVNSDRKTTKLTTNTKLLNSHLMLKTL
          ↑80        ↑90        ↑100       ↑110       ↑120
```

Fig. 5

Lipman-Pearson Protein Alignment
Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>150)	Seq2(1>150)	Similarity	Gap	Gap	Consensus
P123.PRO	EST2P.PRO	Index	Number	Length	Length
(2>148)	(1>146)	21.6	4	5	149

```
                 10        20        30        40        50        60        70        80
P123.PRO  LLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIP
          ::.W:F :L: .:I: FFY TE .: : .Y: R.:.W: ::. I.: K. L.E : :: . .F..:K:R:IP
EST2P.PRO FISWLFRQLIPKIIQTFFYCTEISSTVTIVYF-RHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRIIP
                 10        20        30        40        50        60        70
                 90        100       110       120       130       140       150
P123.PRO  KKT--TFRPIMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVC
          KK: .FR I . : :.: .. K . :. : :: :L. L:N:. .:F. ::: .:: .: .EF
EST2P.PRO KKSNNEFRIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKR-PTSFT-KIYSPTQIADRIKEFKQ
                 80        90        100       110       120       130       140
```

Fig. 6

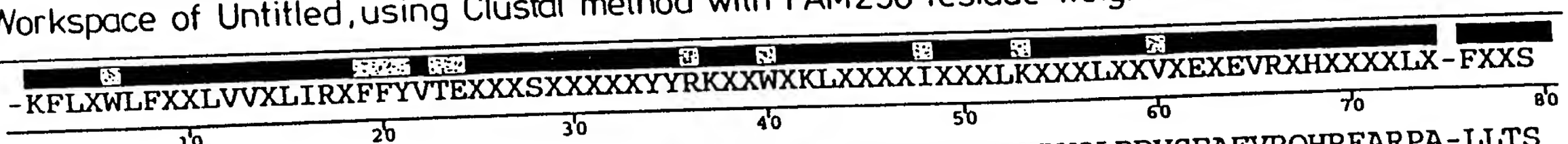
Lipman-Pearson Protein Alignment
Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>129)	Seq2(1>150)	Similarity	Gap	Gap	Consensus
PHTC.PRO	EST2P.PRO	Index	Number	Length	Length
(3>85)	(1>80)	23.3	3	3	83

```
                 10        20        30        40        50        60        70        80
PHTC.PRO  FLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRF
          F: WL..  : .::::FFY TE.:   .  : ::R...W:KL :  I :.:K   L : ::.  .::. : :.:  S::R:
EST2P.PRO FISWLFRQLIPKIIQTFFYCTEIS-STVTIVYFRHDTWNKLITPFIVEYFKTY-LVE-NNVCRNHNSYTLSNFNHSKMRI
                  10        20        30        40        50        60        70
                 90        100       110       120
PHTC.PRO  IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERA
          IPK ..   :     GA .  .  E. .: :::  .:L:Y R.
EST2P.PRO IPKKSNNEFRIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRN
            80        90        100       110       120
```

Fig. 7

Alignment Workspace of Untitled, using Clustal method with PAM250 residue weight table




```
PHTC.PRO   AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPA-LLTS
P123.PRO   -KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEV-EEWKKSLG-FAPG
EST2P.PRO  --FISWLFRQLIPKIIQTFFYCTEIS-STVTIVYFRHDTWNKLITPFIVEYFKTYL---VENNVCRNHNSYTLSNFNHS
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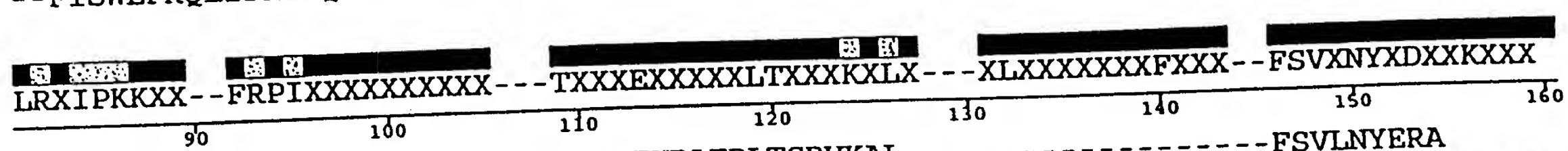


```
PHTC.PRO   LRFIPKPDG--LRPIVNMDYVVGAR---TFRREKRAERLTSRVKAL----------FSVLNYERA
P123.PRO   LRLIPKKTT--FRPIMTFN----KK---IVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYE
EST2P.PRO  MRIIPKKSNNEFR-IIAIPCRGADEEEFTIYKENHKNAIQPTQKILE---YLRNKRPTSFTKI--YSPTQIADRIKEFK
```

Fig. 8

```
GTGCCTGCAG AGACCCGTCT GGTGCACTCT GATTCTCCAC TTGCCTGTTG CATGTCCTCG TTCCCTTGTT    70
TCTCACCACC TCTTGGGTTG CCATGTGCGT TTCCTGCCGA GTGTGTGTTG ATCCTCTCGT TGCCTCCTGG   140
TCACTGGGCA TTTGCTTTTA TTTCTCTTTG CTTAGTGTTA CCCCCTGATC TTTTTATTGT CGTTGTTTGC   210
TTTTGTTTAT TGAGACAGTC TCACTCTGTC ACCCAGGCTG GAGTGTAATG GCACAATCTC GGCTCACTGC   280
AACCTCTGCC TCCTCGGTTC AAGCAGTTCT CATTCCTCAA CCTCATGAGT AGCTGGGATT ACAGGCGCCC   350
ACCACCACGC CTGGCTAATT TTTGTATTTT TAGTAGAGAT AGGCTTTCAC CATGTTGGCC AGGCTGGTCT   420
CAAACTCCTG ACCTCAAGTG ATCTGCCCGC CTTGGCCTCC CACAGTGCTG GGATTACAGG TGCAAGCCAC   490
CGTGCCCGGC ATACCTTGAT CTTTTAAAAT GAAGTCTGAA ACATTGCTAC CCTTGTCCTG AGCAATAAGA   560
CCCTTAGTGT ATTTTAGCTC TGGCCACCCC CCAGCCTGTG TGCTGTTTTC CCTGCTGACT TAGTTCTATC   630
TCAGGCATCT TGACACCCCC ACAAGCTAAG CATTATTAAT ATTGTTTTCC GTGTTGAGTG TTTCTTTAGC   700
TTTGCCCCCG CCCTGCTTTT CCTCCTTTGT TCCCCGTCTG TCTTCTGTCT CAGGCCCGCC GTCTGGGGTC   770
CCCTTCCTTG TCCTTTGCGT GGTTCTTCTG TCTTGTTATT GCTGGTAAAC CCCAGCTTTA CCTGTGCTGG   840
CCTCCATGGC ATCTAGCGAC GTCCGGGGAC CTCTGCTTAT GATGCACAGA TGAAGATGTG GAGACTCACG   910
AGGAGGGCGG TCATCTTGGC CCGTGAGTGT CTGGAGCACC ACGTGGCCAG CGTTCCTTAG CCAGGGTTGG   980
CTGTGTTCCG GCCGCAGAGC ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT  1050
GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC GTTTCAAAAG AACAGGCTCT  1120
TTTTCTACCG GAAGAGTGTC TGGAGCAAGT TGC                                          1153
```

Fig. 9

```
CAGAGCCCTG GTCCTCCTGT CTCCATCGTC ACGTGGGCAC ACGTGGCTTT TCGCTCAGGA CGTCGAGTGG    70
ACACGGTGAT CTCTGCCTCT GCTCTCCCTC CTGTCCAGTT TGCATAAACT TACGAGGTTC ACCTTCACGT   140
TTTGATGGAC ACGCGGTTTC CAGGCACCGA GGCCAGAGCA GTGAACAGAG GAGGCTGGGC GCGGCAGTGG   210
AGCCGGGTTG CCGGCAATGG GGAGAAGTGT CTGGAAGCAC AGACGCTCTG GCGAGGGTGC CTGCAGAGAC   280
CCGCCTGGTG CACTCTGATT CTCCACTTGC CTGTTGCATG TCCTCGTTCC CTTGTTTCTC ACCACCTCTT   350
GGGTTGCCAT GTGCGTTTCC TGCCGAGTGT GTGTTGATCC TCTCGTTGCC TCCTGGTCAC TG           412
```

Fig. 10

```
GGGGTCCTGG GCCCACCCGG GCAGGACGCG TGGACCGAGT GACCGTGGTT TCTGTGTGGT GTCACCTGCC    70
AGACCCGCCG AAGAAGCCAC CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG   140
GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCC TGGGACACGC CTTGTCCCCC   210
GGTGTACGCC GAGACCAAGC ACTTCCTCTA CTCCTCAGGC GACAAGGAGC AGCTGCGGCC CTCCTTCCTA   280
CTCAGCTCTC TGAGGCCCAG CCTGACTGGC GCTCGGAGGC TCGTGGAGAC CATCTTTCTG GGTTCCAGGC   350
CCTGGATGCC AGGGACTCCC CGCAGGTTGC CCCGCCTGCC CCAGCGCTAC TGGCAAATGC GGCCCCTGTT   420
TCTGGAGCTG CTTGGGAACC ACGCGCAGTG CCCCTACGGG GTGCTCCTCA AGACGCACTG CCCGCTGCGA   490
GCTGCGGTCA CCCCAGCAGC CGGTGTCTGT GCCCGGGAGA AGCCCCAGGG CTCTGTGGCG GCCCCCGAGG   560
AGGAGGACAC AGACCCCCGT CGCCTGGTGC AGCTGCTCCG CCAGCACAGC AGCCCCTGGC AGGTGTACGG   630
CTTCGTGCGG GCCTGCCTGC GCCGGCTGGT GCCCCCAGGC CTCTGGGGCT CCAGGCACAA CGAACGCCGC   700
TTCCTCAGGA ACACCAAGAA GTTCATCTCC CTGGGGAAGC ATGCCAAGCT CTCGCTGCAG GAGCTGACGT   770
GGAAGATGAG CGTGCGGGAC TGCGCTTGGC TGCGCAGGAG CCCAGGTGAG GAGGTGGTGG CCGTCGAGGG   840
CCCAGGCCCC AGAGCTGAAT GCAGTAGGGG CTCAGAAAAG GGGGCAGGCA GAGCCCTGGT CCTCCTGTCT   910
CCATCGTCAC GTGGGCACAC GTGGCTTTTC GCTCAGGACG TCGAGTGGAC ACGGTGATCT CTGCCTCTGC   980
TCTCCCTCCT GTCCAGTTTG CATAAACTTA CG                                           1012
```

Fig. 11

```
GAATTCGCGG CCGCGTCGAC GTTTCAGGCA GCGCTGCGTC CTGCTGCGCA CGTGGGAAGC CCTGGCCCCG 70
GCCACCCCCG CGATGCCGCG CGCTCCCCGC TGCCGAGCCG TGCGCTCCCT GCTGCGCAGC CACTACCGCG 140
AGGTGCTGCC GCTGGCCACG TTCGTGCGGC GCCTGGGGCC CCAGGGCTGG CGGCTGGTGC AGCGCGGGGA 210
CCCGGCGGCT TTCCGCGCGC TGGTGGCCCA GTGCCTGGTG TGCGTGCCCT GGGACGCACG GCCGCCCCCC 280
GCCGCCCCCT CCTTCCGCCA GGTGTCCTGC CTGAAGGAGC TGGTGGCCCG AGTGCTGCAG AGGCTGTGCG 350
AGCGCGGCGC GAAGAACGTG CTGGCCTTCG GCTTCGCGCT GCTGGACGGG GCCCGCGGGG GCCCCCCCGA 420
GGCCTTCACC ACCAGCGTGC GCAGCTACCT GCCCAACACG GTGACCGACG CACTGCGGGG GAGCGGGGCG 490
TGGGGGCTGC TGCTGCGCCG CGTGGGCGAC GACGTGCTGG TTCACCTGCT GGCACGCTGC GCGCTCTTTG 560
TGCTGGTGGC TCCCAGCTGC GCCTACCAGG TGTGCGGGCC GCCGCTGTAC CAGCTCGGCG CTGCCACTCA 630
GGCCCGGCCC CCGCCACACG CTAGTGGACC CCGAAGGCGT CTGGGATGCG AACGGGCCTG GAACCATAGC 700
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AGAAAAGGAC TCCCAAGGAC TGGACCTTTC GCCGAAGCCC CTGGAGCAGA CACCAGGGGT CAAACCAACC 3290
TTCGTCCTCC ATCCCATAAG ACGCCAAAGC CACTCCCTCT GTGTTTATCC AGGGAAACTT GTTCCGAAGC 3360
TGATCAGGAG ACATCAGAGA AACTTTGGCT CCCTCCTGCC TCTGCACTTT CACGTTGCTC TCCATGGCTG 3430
CAGCATCCTT TTCTGAAGCC AGCAAGAGGT AGCCCGAGGG GTTGAACCGG AGGTCCAGGG GAGGAGCATC 3500
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GTTCCACCAC TAGCACTCGA ATAGCACCTC GTCTGCTCTC CAGCTTCTTC AGCCAATAGG CCACAGACAA 3710
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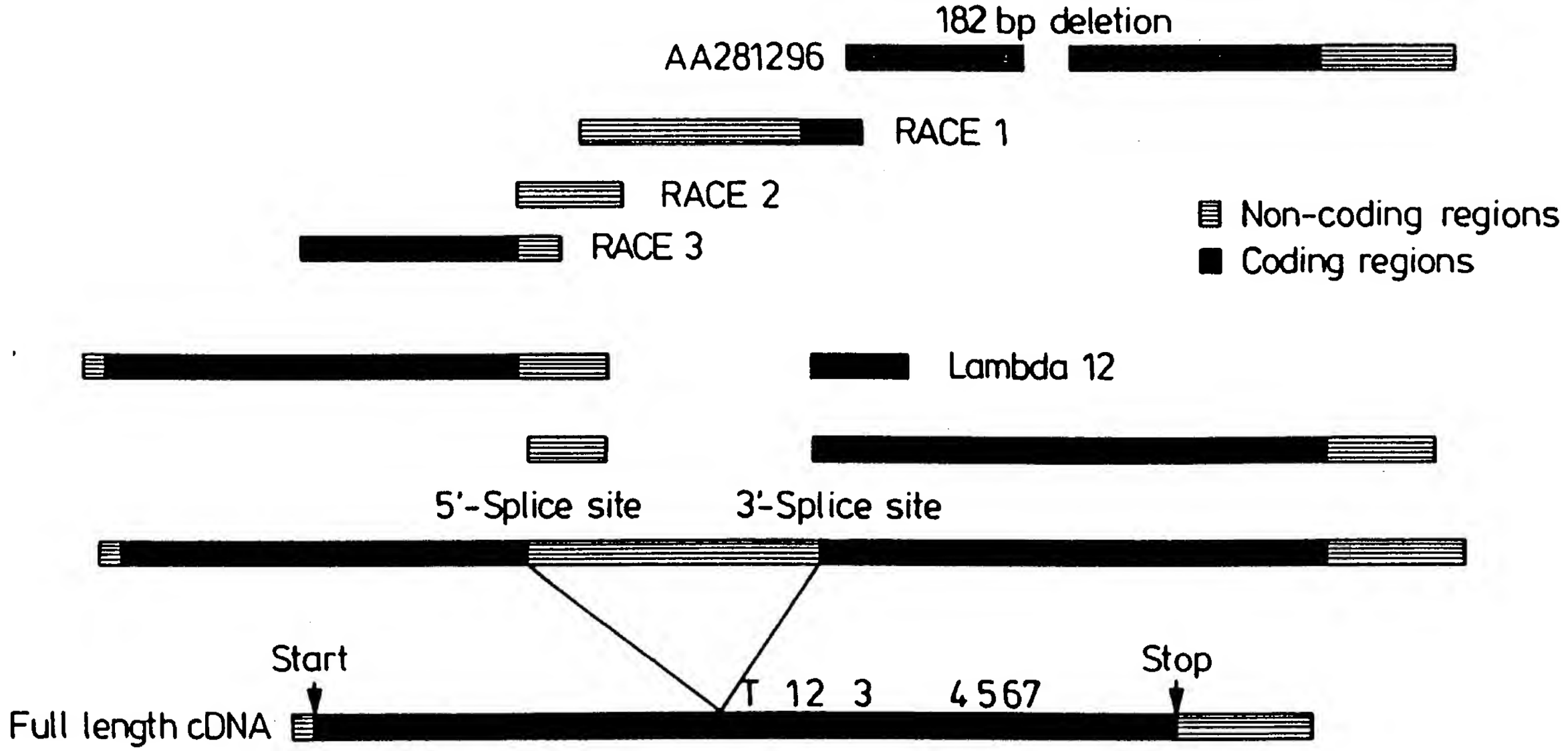
Fig. 12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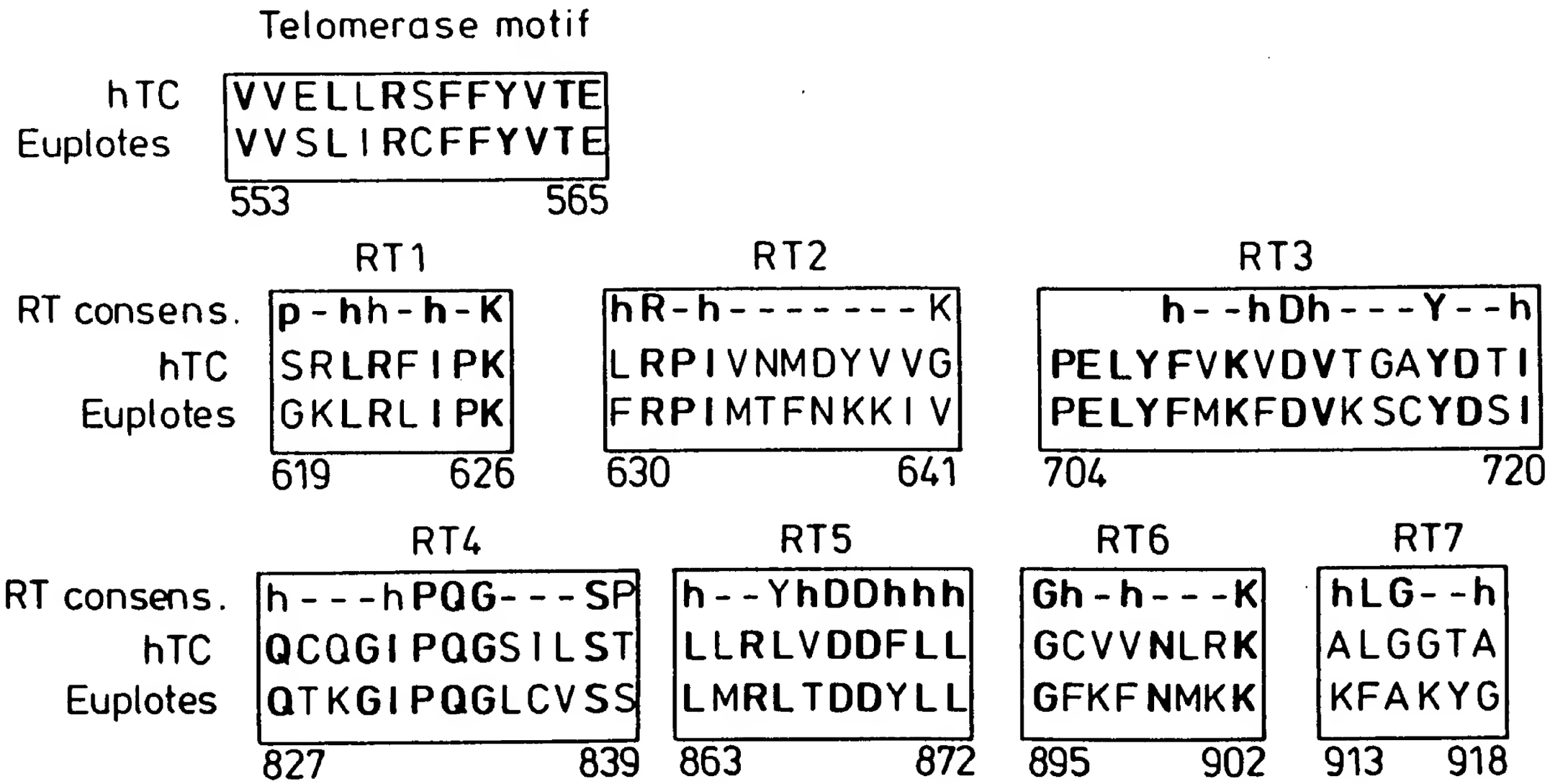
AA281296
RACE 1
RACE 2
RACE 3
Non-coding regions
Coding regions
Lambda 12
5'-Splice site
3'-Splice site
Start
Stop
T 12 3 4567
Full length cDNA

Fig.13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Euplotes VVSLIRCFFYVTE
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RT2
RT3
RT consens. p-hh-h-K
hTC SRLRFIPK
Euplotes GKLRLIPK
619 626
hR-h-------K
LRPIVNMDYVVG
FRPIMTFNKKIV
630 641
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704 720
RT4
RT5
RT6
RT7
RT consens. h---hPQG---SP
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LMRLTDDYLL
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913 918

Fig. 14

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TCATCCCCAA GCCTGACGGG CTGCGGCCGA TTGTGAACAT GGACTACGTC GTGGGAGCCA GAACGTTCCG   1993
CAGAGAAAAG AGGGCCGAGC GTCTCACCTC GAGGGTGAAG GCACTGTTCA GCGTGCTCAA CTACGAGCGG   2063
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Fig. 15

Fig. A

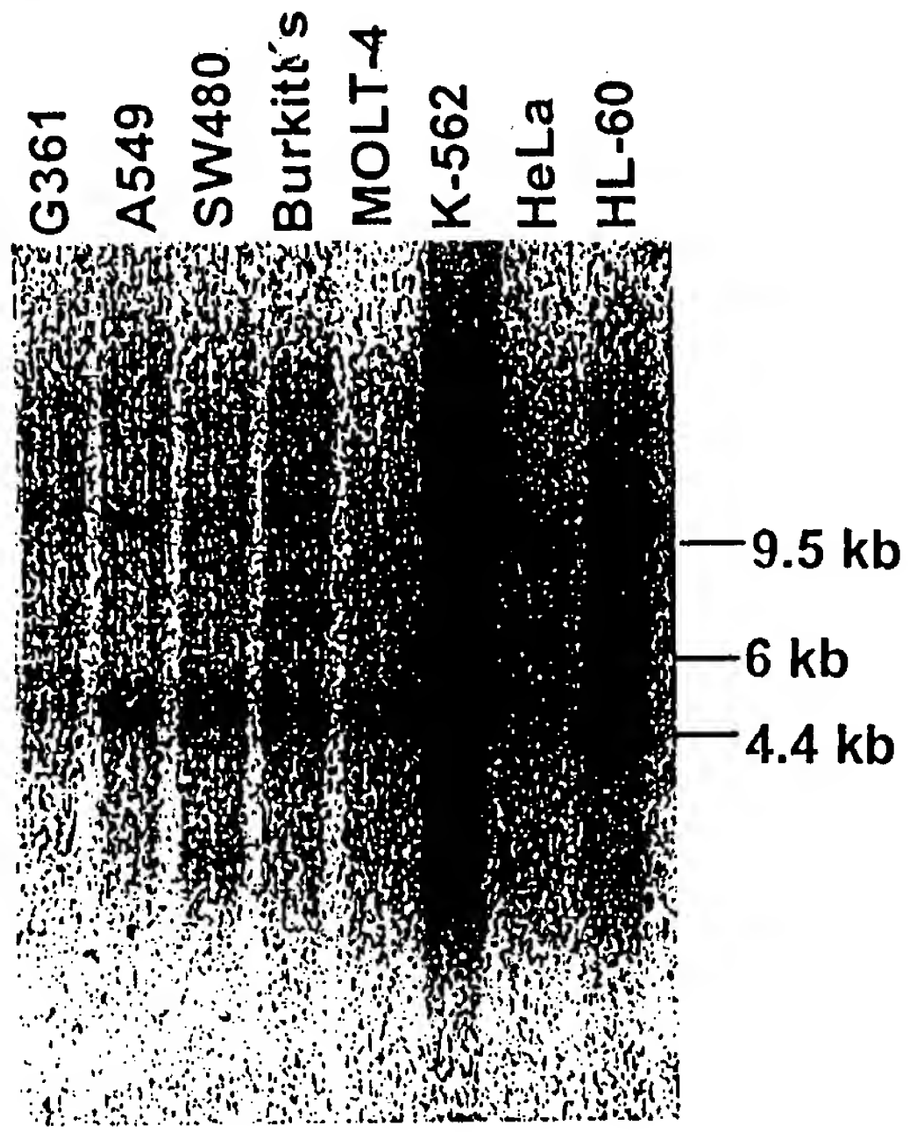


Fig. B

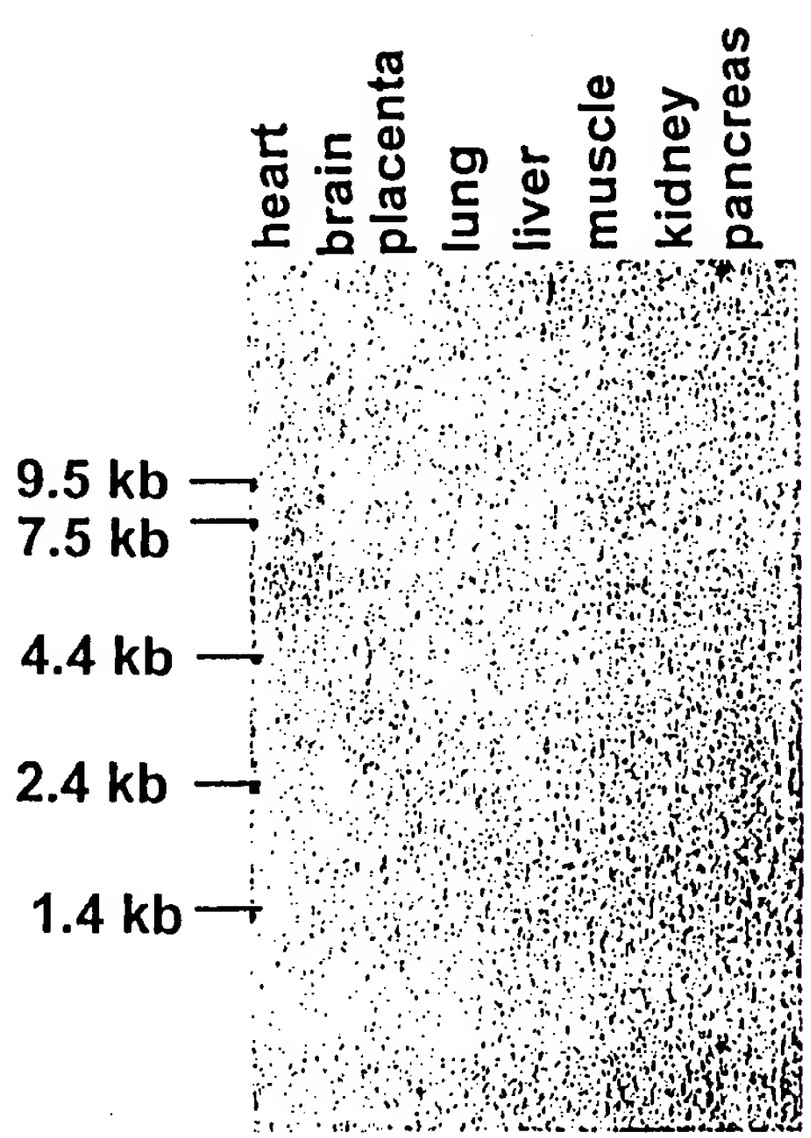
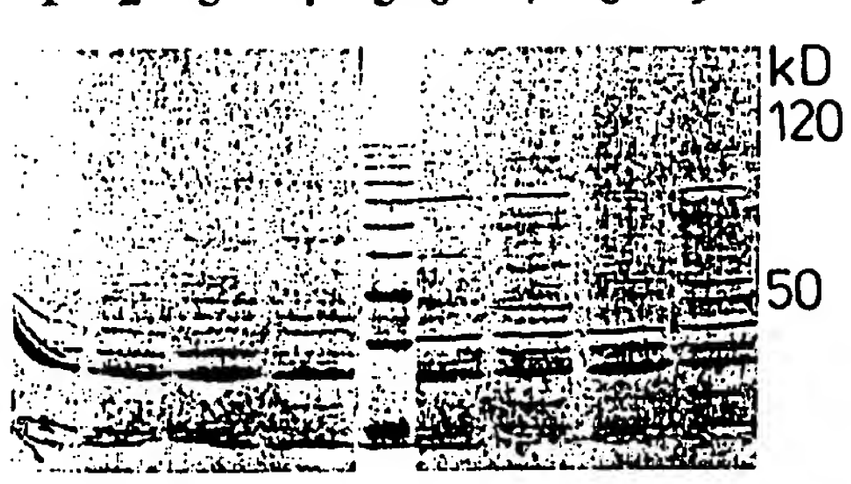


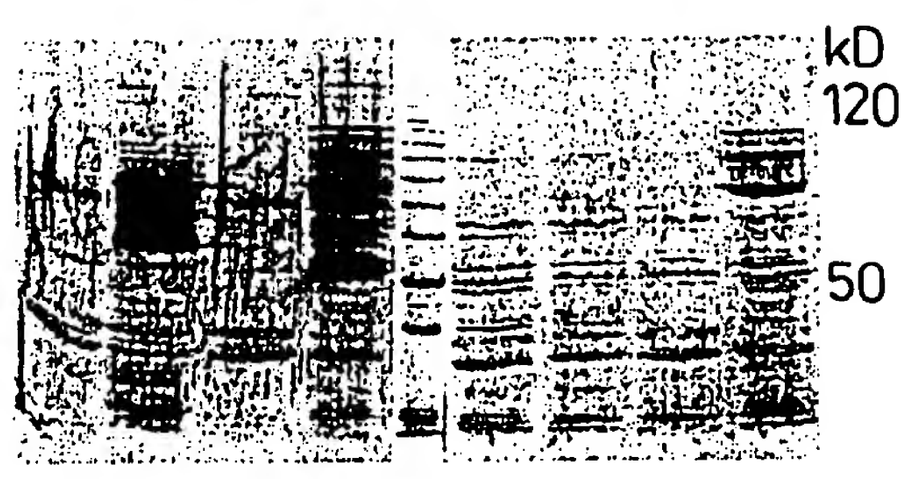
Fig. 16

Fig. A



pMAL EST	pMAL-EST	pMAL AI	pMal AI	M	pMAL-EST	pMAL-EST	pMAL AI	pMAL AI
-	+	-	+		-	+	-	+
anti-B pre-immun					anti-C pre-immun			

Fig. B



pMAL-EST	pMAL-EST	PMAL AI	pMAL AI	M	pMAL-EST	pMAL-EST	pMAL AI	pMAL AI
-	+	-	+		-	+	-	+
anti-B 1° immun.					anti-C 1° immun.			

09/424686

Fig. 17

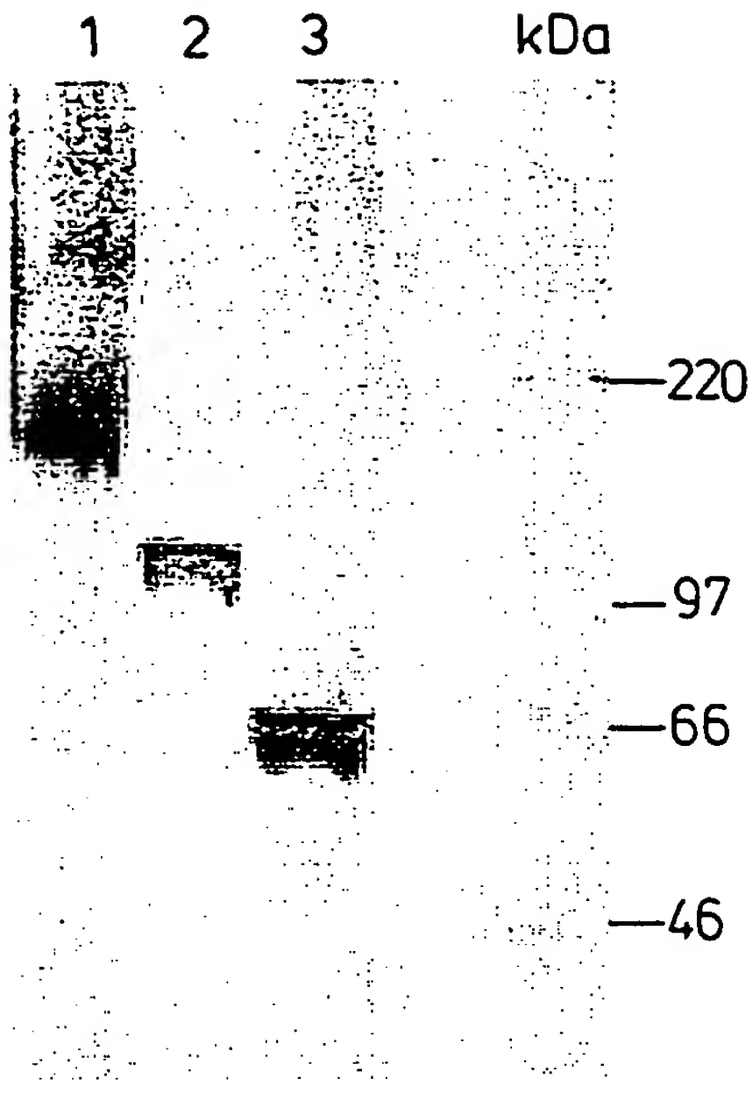


Fig. 18

Fig. 19